

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

CLAIM AMENDMENTS

1. *(Currently Amended)* A method of identifying a nucleic acid that encodes human telomerase reverse transcriptase (hTERT) or fragment thereof in a sample, comprising:
 - a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes ~~human telomerase reverse transcriptase (hTERT)~~ hTERT or fragment thereof;
 - b) detecting any hybrid formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the hybrid is detected;wherein the probe hybridizes specifically to a DNA having the sequence of the hTERT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;
wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.
2. *(Currently Amended)* A method of detecting a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
 - a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO:224 if present in the sample; and
 - b) detecting any hybrid formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the hybrid is detected;wherein the polynucleotide probe consists essentially of a sequence identical or complementary to 25 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
3. *(Original)* The method of claim 2, wherein the hTERT nucleic acid is human genomic DNA.
4. *(Previously presented)* The method of claim 2, wherein the hTERT nucleic acid is mRNA or cDNA.
5. *(Currently Amended)* The method of claim 2, wherein the hTERT nucleic acid ~~comprises~~ consists essentially of 250 or more nucleotides of SEQ ID NO:224.
6. *(Currently Amended)* The method of claim 2, wherein the hTERT nucleic acid ~~comprises~~ consists essentially of 500 or more nucleotides of SEQ ID NO:224.

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7. *(Currently Amended)* The method of claim 2, wherein the probe ~~comprises~~ consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
8. *(Currently Amended)* The method of claim 2, wherein the probe ~~comprises~~ consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
9. *(Currently Amended)* The method of claim 2, wherein the probe ~~comprises~~ consists essentially of a sequence identical or complementary to 100 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
10. *(Original)* The method of claim 2, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.
11. *(Original)* The method of claim 9, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.
12. *(Original)* The method of claim 2, wherein the sample is a human biological sample.
13. *(Currently Amended)* A method of identifying a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
 - a) combining the sample with a polynucleotide primer under conditions that the primer specifically primes amplification of ~~the nucleic acid if the nucleic acid encodes human telomerase reverse transcriptase (hTERT)~~ SEQ. ID NO:224 or fragment thereof if present in the sample;
 - b) detecting any amplification product formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the amplification product is detected;wherein the primer hybridizes specifically to a DNA having the sequence of the hTERT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;
wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

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14. *(Currently Amended)* A method of detecting a nucleic acid encoding hTERT or fragment thereof in a sample, comprising:
- a) combining the sample with polynucleotide primers so as to prime amplification of nucleic acid encoding hTERT or fragment thereof if present in the sample; ~~and~~
 - b) detecting any amplified product formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the amplification product is detected;
- wherein ~~the~~ each of said primers consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
15. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
16. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
17. *(Original)* The method of claim 14, wherein the sample is a human biological sample.
18. *(Original)* The method of claim 14, wherein the sample comprises human genomic DNA.
19. *(Previously presented)* The method of claim 14, wherein the sample comprises hTERT mRNA or cDNA.
20. **CANCELLED.**
21. *(Original)* The method of claim 14, wherein the primers comprise a sequence not contained in SEQ. ID NO:62.
22. **CANCELLED**
23. *(Withdrawn)* A combination of oligonucleotide primers for PCR amplification for use in detecting an hTERT nucleic acid according to claim 14, wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.

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24. *(Withdrawn)* The combination of primers of claim 23, wherein each primer consists of 15-30 nucleotides.

25. *(Withdrawn)* The combination of primers of claim 23, wherein each primer consists of 20-25 nucleotides.

26. *(Withdrawn)* The combination of primers of claim 23, wherein 50% or more of the nucleotides of each primer are guanine and/or cytosine.

27 to 34. *CANCELLED*

35. *(Previously presented)* The method of claim 1, wherein a) comprises combining the sample with the probe at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.

36. *(Previously presented)* The method of claim 1, wherein the hTERT nucleic acid is hTERT mRNA or cDNA.

37. *(Previously presented)* The method of claim 1, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.

38. *(Currently Amended)* The method of claim 1, wherein the ~~probe comprises a sequence~~ nucleic acid sequence of the probe is not contained in SEQ. ID NO:62.

39. *(Currently Amended)* The method of claim 1, wherein the sample has been taken from a patient ~~, and the method further comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTERT or an hTERT fragment is detected~~ having a tumor.

40. *(Currently Amended)* The method of claim 2, wherein the sample has been taken from a patient ~~, and the method further comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTERT or an hTERT fragment is detected~~ having a tumor.

41. *(Previously presented)* The method of claim 13, wherein a) comprises combining the sample with the primer at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.

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42. *(Previously presented)* The method of claim 13, wherein the hTERT nucleic acid is mRNA or cDNA.
43. *(Previously presented)* The method of claim 13, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ ID NO:224.
44. *(Previously presented)* The method of claim 13, wherein the primer comprises a sequence not contained in SEQ. ID NO:62.
45. *(Currently Amended)* The method of claim 13, wherein the sample has been taken from a patient ~~, and the method comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTERT or an hTERT fragment is detected~~
having a tumor.
46. *(Currently Amended)* The method of claim 14, wherein the sample has been taken from a patient ~~, and the method comprises determining or assessing a tumor in the patient according to whether said amplification product is formed~~
having a tumor.